subcontinent, it has its highest diversity in southern Africa. The genus was first described by E. Meyer in 1838 and at the time consisted of only three species: *A. biflorum, A. heterophyllum* and *A. fasciculare*. These were subsequently all moved to *Schizoglossum* by R. Schlechter (1894–1895). In 1984, Kupicha re-instated the genus and enlarged it to 34 species by adding six new species to the original three of Meyer and twenty-five species which have basionyms in *Schizoglossum*. She also divided the genus into four sections namely sect. *Aspidoglossum*, sect. *Latibrachium*, sect. *Verticillus* and sect. *Virga*. Since Kupicha's revision two new species have been added to the genus. The genus (sensu Kupicha) is thought to be closely related to *Schizoglossum* but distinguished from it by the sessile, fasciculate inflorescences, and sausage-shaped pollinia which are sub-apically attached to the corpusculum and equipped with a well-developed germination zone. The species are all perennial herbs with milky latex in all parts. Flowering shoots are produced annually which die back or are burnt to ground level. The plants survive as an underground spindle-shaped tuber. The first author is currently studying *Schizoglossum* sens. lat. and allied groups which include *Aspidoglossum*. In this overview the genus is grouped into the current four sections. The distribution of the species, flower morphology, diagnostic characters and a synopsis of species are presented. A number of new species are in the process of being described and some synonyms will be re-instated.

P0740 – ePoster

The Pl@ntnet project: plant computational identification and collaborative information system

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Among the world's living species, there are approximately 300,000 species of plants. Accurate knowledge of their identity, geographic distribution and use, underpins the success of the world sustainable agriculture with advanced research in agronomy, and biodiversity conservation. Unfortunately, the quality and quantity of plant information is poorest in the regions that could use it the most: Mediterranean and tropical countries. It's for this reason that plant identification, sharing of and access to plant information play a crucial but little understood role in modern society. In this context, Agropolis Fondation (http://www.agropolis-fondation.fr/) is supporting its first Flagship Programme called Pl@ntNet. This programme involves a large international partnership jointly led by the AMAP Joint Research Unit (http://umramap.cirad.fr), the IMEDIA Research Team (http://www-rocq.inria.fr/imedia/), and the non-governmental organization Tela Botanica (http://www.tela-botanica.org/). The Pl@ntNet project aims to set up a web-oriented scientific, informative and educational software platform dedicated to plant identification and to the collaborative gathering, share and use of large, multi-disciplinary datasets on plants. Free, open-source, easy-access software programs, based on previously developed prototypes will function on-line on internet, or directly in the field, and will be adapted to the various working conditions of potential users (natural resources managers, foresters, agronomists, teachers, scientists or citizens). Plant identification tools will be based on the use of morphological, ecological or geographical characters, as well as on visual image recognition system. As an initiative of major scientific and strategic importance, Pl@ntNet is expected to bring scientific breakthrough and demonstrate the degree and extent by which the know-how, expertise and competencies of various research units and their partners are mobilized and put into use in order to contribute in addressing major challenges of our time.

P0743 – ePoster

Genome-level evidence of adaptive variation among natural eucalypt populations: implications for evolution and conservation

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Understanding the genetic basis of local adaptation, together with identifying ecologically relevant genomic regions, is a major goal of evolutionary, ecological and conservation genetics. By understanding adaptation at the genomic level we can answer questions about i) species evolution, ii) conservation management of contemporary gene-pools, and of ecological and evolutionary processes, iii) predicting species' responses to climate change, and iv) the nature of environmental drivers of adaptation. Simple, rapid methods for identifying adaptation at the genome level are rare, especially for natural populations of non-model species, but the increasing amount of whole-genome information for *Eucalyptus* has allowed us to investigate new methods for detecting evidence of natural selection. Our aims in this study are to: i) develop gene-associated microsatellite markers that occur within *Eucalyptus* expressed sequence tags (ESTs); ii) predict the phenotypic function of those regions by sequence homology with known genes; iii) compare genetic structure and diversity measured with neutral microsatellites versus gene-linked EST-microsatellites; iv) perform statistical tests for natural selection; and v) establish the first reciprocal transplant field trial of our study species to assess variation in quantitative traits. The study species is *Eucalyptus gomphocephala* (*Symphyomyrtus*), a forest and woodland tree of ecological value and conservation concern native to the coastal plain of southern Western Australia. We designed and optimised PCR primers for 11 microsatellite loci within *Eucalyptus* ESTs that are homologous with genes involved in flowering time (CONSTANS), pathogen defence (β-1,3-glucanase), heat shock (HSF), photosynthesis (chlorophyll A/B binding protein), desiccation protection (Lea14) and others. Through Bayesian Fst outlier tests and other statistical methods, we will test for signatures of natural selection at these loci, and based on the sequence homology, will predict the environmental factors that may be involved in the adaptive process. The 1.5 year-old reciprocal transplant